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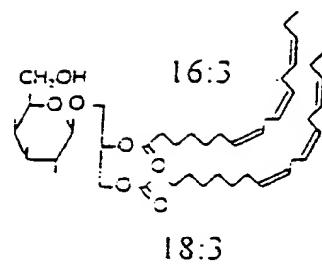


FIGURE 1

A

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sOMGD A MSHPST/TSEPSN-LLDFV/KLGNFVLNSSLHGNNSNGYSSSSNSVHFGGLAT---QN 55
 cSMGD A MRNPSTV/QENGS-V3CFISCLGYFAFSSRFLVNLNS2CGSGSSSHSLYLNQFENYRC-KP 59
 acMGD A MQNPSTV/TQESAAPVDFPPRLRGLTSRNRSPCSNSDGYALSSSNALYFNGFRTPS-RR 59
 acMGD B ----- 0

 sOMGD A RYKFVNLSF---SK2GSNLKRLISDFNRVIRLHCDRI-PLGFSSICLN--SGESNGVSD 109
 cSMGD A PPRSGASLSSL-SRGSSSLRRLFVNEFNNVIKFHCHKP-PLGFASLCCV--SDETNIGRD 114
 acMGD A MGKTLASLSFNTKSSAGSSLRRFISDFNSFIRFHCDCKVPPESFASVGGVGLSSDENIRE 119
 acMGD B ---MATTVM---ALA2KVLERVYGTSGSAVSVTSGDGEKTHRHTHRIKSYCIDE 51

 sOMGD A NGHS-VLEDVRVPVNA2PEPSKRVLILMSDTCGGHRASAEAIKAFAFNEEFQDDYQVFVT 168
 cSMGD A DFGC-VSDGCLPLNKIEAENPKRVLILMSDTCGGHRASAEAIKAFAFNEEFQNNYQVFIT 173
 acMGD A NGTGGVLLGEGGLPLNGTCAORPKVVLILMSDTCGGHRASAEAIKAFAFNEEFQDGYQVFIT 179
 acMGD B DESS-----LELIOIGAERTQVILILMSDTCGGHRASAEAIKAFAFNEEFQDGYQVFIT 106

 sOMGD A DLWSEHTPWPFPNQLPRTSYNFLVKGPLWKNMYYGTSPrVHQSNSFAATSVFIARESVARGL 228
 cSMGD A DLWTEHTPWPFPNCLPRTSYNFLVKGTLWKNMYYTAPKVIHQSNSFAATSTFIAREVAKGL 233
 acMGD A DLWTDKTPWPFPNCLPRTSYNFLVKGTLWKNMYYGTSPrVHQSNSFAATSTFIAREIAAGGL 239
 acMGD B DVWKEYTGWPLNDMERSYKFMVQGVOLWVKAHISTSPGTHSCYLAAIAAAYAKEVEAGL 166

 sOMGD A MKYOPDIIISVHPLMCHVPLRILRGRGLLEKIVFTTITDLSCHPTWFKLVTRCYCP 293
 cSMGD A MKYRPDIIISVHPLMCHVPLRIRSKGLLNKCVFTTITDLSCHPTWFKLVTRCYCP 293
 acMGD A MKYOPDIIISVHPLMCHVPLRVLRSKGLLKKIVFTTITDLSCHPTWFKLVTRCYCP 299
 acMGD B MEYKPEIIISVHPLMQH1PLWV/LKQELQKRVLFVTVITDLSCHPTWFKLVTRCYCP 226

 sOMGD A NEVAKRATKAGLOPSOIKEYGLPVRPSFVRSPRKQNEELRKELGMDEHLPAVLLMGGEGM 348
 cSMGD A TEVAKRATLAGLOPSKLK/FGLPVRPSFVKP1R9K1ELRKELGMDEHLPAVLLMGGEGM 353
 acMGD A TEVAKRAGKACLETSGIKEYGLPVRPSFVKPVRPK/ELRRELGMDEHLPAVLLMGGEGM 359
 acMGD B QEVAKRAL/FGGLDESQVRVFGLPVRPSFARAVLVIDLRKELEMDDQLRAVLLMGGEGM 286

 sOMGD A GPEIATARALGNALYDANLGEPTGCOLLVIICSRNICKLACKLSSLDWKIPVQVKGFVTKIIS 408
 cSMGD A GPEIATAKAALSALYDANHGE2P1GQVLV123HNNKKLACRLRSIDDWKPVQVKGFVTKIIS 413
 acMGD A GPEIATARALADALYD1K1GEAVGQVLLIICSRNICKLSSLDWKIPVQVKGFVTKIIS 419
 acMGD B GPVKETAKALEEFLYD1K1RKP1GGMV123RNNKKLSSLDWKIPVQVKGFVTKIIS 345

 sOMGD A CMGACDCIITKAGPGTIAEAMIRGLPIILNDYIAGOEAQNVPYVITENGIGKYLKSPKEIA 468
 cSMGD A CMGACDCIITKAGPGTIAEAMIRGLPIILNDYIAGOEAQNVPYVYENCGKFSKSPKEIA 471
 acMGD A CMGACDCIITKAGPGTIAEAMIRGLPIILNDYIAGOEAQNVPYVYENCGKFSKSPKEIA 479
 acMGD B WMGACDCIITKAGPGTIAEASLIRSLPIILNDYIPGQEKGNVNPYVYENAGVFRSPKETA 406

 sOMGD A KTV5QWFGPKANELIMSONALKHPDAVFKIVHDLDELVRQKIFVRCYSCAA----- 522
 cSMGD A NIVAKWFGPKADELLIMSONALR1RPAVFKIVHDLHELVKQRSFVQYSG----- 525
 acMGD A KIVADWFGPKASKELEIMSONALR1LAKPEAVFKIVHDMKELVRK1KNSLPOLSCTA----- 533
 acMGD B RIVGEWFSTKTDLEQTSNDNARKLAQPEAVFDIVKDIELSEQRGP LASVSYNLTSSFASLV 468

h7

B

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_____ sOMGD A
 _____ cSMGD A
 _____ acMGD A
 _____ acMGD B

FIGURE 2

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A

B

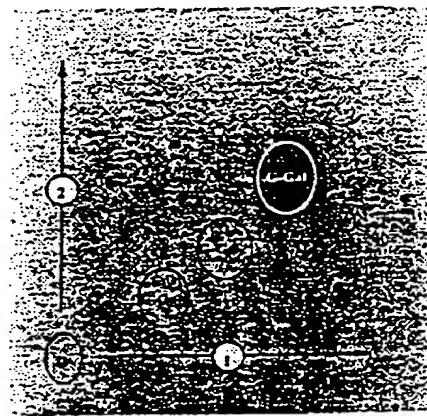
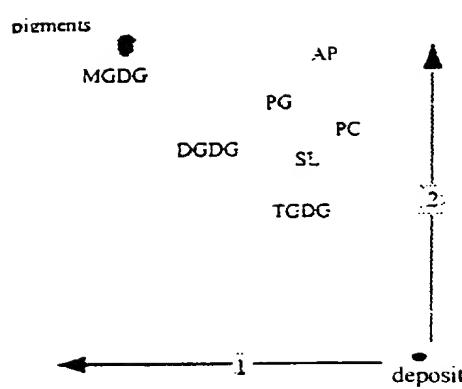


FIGURE 3

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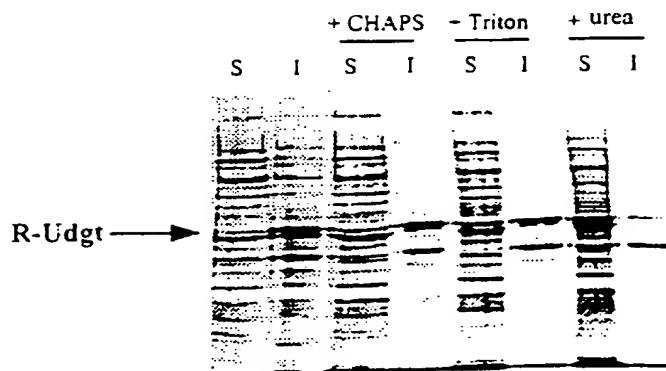
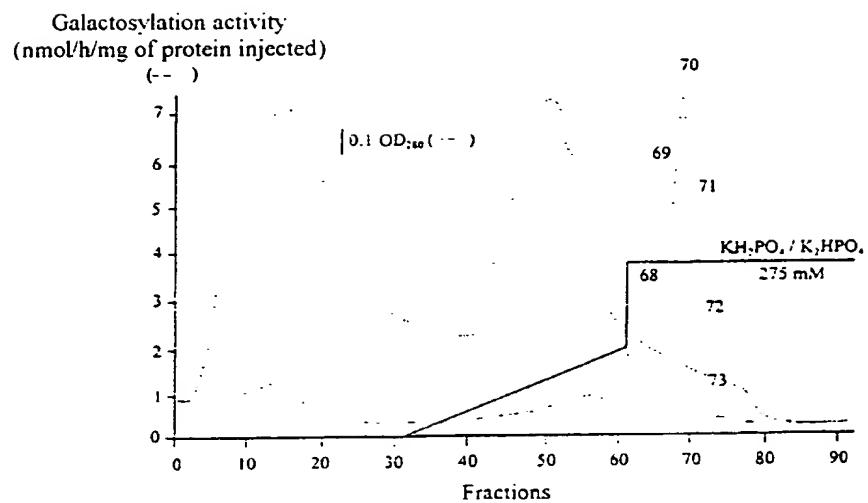
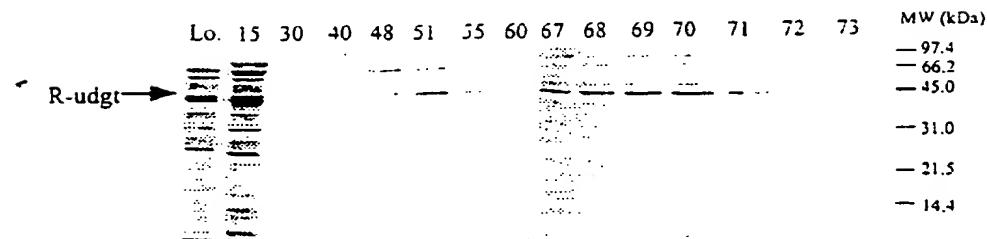


FIGURE 4

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FIGURE 5AFIGURE 5B